

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representation of
The original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

BEST AVAILABLE COPY**BEST AVAILABLE COPY**

Point of Contact:

Jan Delaval
Librarian-Physical Sciences
CM1-TE01 Tel: 308-4498**STAFF USE ONLY**Searcher: JanSearcher Phone #: 4498Searcher Location: Room 2205Date Searcher Picked Up: 12/18Date Completed: 12/18

Searcher Prep & Review Time: _____

Clerical Prep Time: 10Online Time: 10**Type of Search**

NA Sequence (#) _____

AA Sequence (#) ✓

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis/Nexis _____

Sequence Systems ✓

WWW/Internet _____

Other (specify) _____

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:21 ; Search time 12.49 seconds
(without alignments)
1118.439 Million cell updates/sec

Title: US-09-555-473-1

Perfect score: 2007

Sequence: 1 MHLLALFCAWSAVLAENS.....NIVGWGVTQPHGGAQYVS 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

al number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2007	100.0	381	1 PTX3_HUMAN	P26022 homo sapien
2	1667	83.1	381	1 PTX3_MOUSE	P48759 mus musculus
3	296.5	14.8	427	1 APEX_CAVPO	P47970 cavia porce
4	295.5	14.7	430	1 NPX2_HUMAN	P47972 homo sapien
5	289	14.4	432	1 NPX1_RAT	P47971 rattus norv
6	287	14.3	432	1 NPX1_MOUSE	Q62443 mus musculus
7	281	14.0	430	1 NPX1_HUMAN	Q15818 homo sapien
8	256.5	12.8	242	1 CRP4_LIMPO	P06206 limulus pol
9	249.5	12.4	242	1 CRP3_LIMPO	P06207 limulus pol
10	248.5	12.4	242	1 CRP1_LIMPO	P06205 limulus pol
11	225.5	11.2	230	1 CRP_RAT	P48199 rattus norv
12	218.5	10.9	416	1 PXN1_XENLA	P49263 xenopus lae
13	217.5	10.8	225	1 CRP_MESAU	P49262 mesocricetu
14	212.5	10.6	231	1 FP_CRIMI	P15697 cricetus
15	203.5	10.1	225	1 CRP_MOUSE	P14847 mus musculus
16	199.5	9.9	225	1 CRP_RABIT	P02742 oryctolagus
17	192.5	9.6	234	1 CRP_CAVPO	P49254 cavia porce
18	187.5	9.3	234	1 SAMP_MESAU	P07629 mesocricetu
19	184.5	9.2	224	1 CRP_HUMAN	P02741 homo sapien
20	181	9.0	238	1 CRP_XENLA	Q07203 xenopus lae
21	179.5	8.9	228	1 SAMP_RAT	P23680 rattus norv
22	166	8.3	224	1 SAMP_MOUSE	P12246 mus musculus
23	164.5	8.2	223	1 SAMP_CAVPO	P49255 cavia porce
24	161.5	8.0	223	1 SAMP_HUMAN	P02743 homo sapien
25	112.5	5.6	899	1 PRO6_YEAST	P19735 saccharomyc
26	99.5	5.0	651	1 PRIA_MYCLE	Q9ccq3 mycobacteri
27	99	4.9	304	1 MMGL_MOUSE	P49300 mus musculus
28	97.5	4.9	412	1 NEMO_MOUSE	O88522 m nf-kappab
29	97	4.8	1170	1 XPG_MOUSE	P35689 mus musculus
30	95	4.7	284	1 TPW1_BIOGL	P42636 biomphalari
31	94	4.7	527	1 HSF8_LYCES	Q40152 lycopersico
32	92.5	4.6	284	1 TPW2_BIOGL	P43689 biomphalari
33	92	4.6	306	1 MMGL_RAT	P49301 rattus norv

34	92	4.6	866	1 NASA_KLEPN	Q05457 klebsiella
35	92	4.6	958	1 VIA_CCMV	P27752 cowpea chlo
36	91.5	4.6	230	1 Y966_MYCTU	P71544 mycobacteri
37	91.5	4.6	280	1 STO2_CAEEL	Q19958 caenorhabd
38	91	4.5	864	1 AKA3_MOUSE	O89887 mus musculu
39	90.5	4.5	527	1 HSF8_LYCPPE	P41153 lycopersico
40	90.5	4.5	1969	1 MYSA_CAEEL	P12844 caenorhabd
41	90.5	4.5	2035	1 EVPL_MOUSE	Q9d952 mus musculu
42	90.5	4.5	5430	1 ACF7_HUMAN	Q9upn3 homo sapien
43	90	4.5	283	1 LECH_RAT	P02706 rattus norv
44	90	4.5	330	1 Y677_METJA	Q58090 methanococc
45	89.5	4.5	1487	1 ICP4_HSVK	P17473 equine herp

ALIGNMENTS

RESULT 1
PTX3_HUMAN
ID PTX3_HUMAN STANDARD; PRT; 381 AA.
AC P26022;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR-
DE INDUCIBLE PROTEIN TSG-14).
GN PTX3 OR TSG14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=93054498; PubMed=1429570;
RA Breviario F., D'Aniello E.M., Golay J., Peri G., Bottazi B.,
RA Bairoch A., Saccone S., Marzella R., Predazzi V., Rocchi M.,
RA della Valle G., Dejana E., Mantovani A., Introna M.;
RT Interleukin-1-inducible genes in endothelial cells. Cloning of a new
RT gene related to C-reactive protein and serum amyloid P component.*;
RL J. Biol. Chem. 267:22190-22197(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=94178310; PubMed=8131794;
RA Introna M., Breviario F., D'Aniello E.M., Golay J., Dejana E.,
RA Mantovani A.;
RT IL-1 inducible genes in human umbilical vein endothelial cells.*;
RL Eur. Heart J. 14:78-81(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fore skin;
RX MEDLINE=93171605; PubMed=7679696;
RA Lee G.W., Lee T.H., Vilcek J.;
RT TSG-14, a tumor necrosis factor- and IL-1-inducible protein, is a
RT novel member of the pentaxin family of acute phase proteins.*;
RL J. Immunol. 150:1804-1812(1993).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=95015860; PubMed=7523502;
RA Lee G.W., Goodman A.R., Lee T.H., Vilcek J.;
RT Relationship of TSG-14 protein to the pentaxin family of major
RT acute phase proteins.*;
RL J. Immunol. 153:3700-3707(1994).
CC -!- INDUCTION: BY INTERLEUKIN-1 BETA AND TNF-ALPHA.
CC -!- PTM: GLYCOSYLATED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

CC EMBL; X63053; CAA44778.1; -;
CC EMBL; X63613; CAA45158.1; -;
CC EMBL; M31166; AAA61234.1; -;
CC PIR; S18947; S18947.
CC PIR; S17069; S17069.
CC PIR; A44323; A44323.
CC MIM; 602492; -;
CC InterPro; IPR001759; Pentaxin.
CC Pfam; PF00354; pentaxin; 1.
CC PRINTS; PR00895; PENTAXIN.
CC SMART; SM00159; PTX; 1.
CC PROSITE; PS00289; PENTAXIN; 1.
CC Pentaxin; Glycoprotein; Signal.
CC SIGNAL 1 17 POTENTIAL.
CC CHAIN 18 381 PENTAXIN-RELATED PROTEIN PTX3.
CC DOMAIN 183 381 PENTAXIN.
CC DISULFID 210 271 BY SIMILARITY.
CC CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 202 202 M -> L (IN REF. 3).
CC SEQUENCE 381 AA; 42019 MW; 787F749DBC6D59B CRC64;

Query Match 100.0%; Score 2007; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHLAIFCALWSAVLAENSDDDYDLMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
DB 1 MHLAIFCALWSAVLAENSDDDYDLMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
QY 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAGAPAPARLTSALDEL 120
DB 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAGAPAPARLTSALDEL 120
QY 121 LOATRDAGRRLARMEGAEOPEAGRALAAVLEELRQTRADLHAYOGVAARSWLPAGCE 180
DB 121 LOATRDAGRRLARMEGAEOPEAGRALAAVLEELRQTRADLHAYOGVAARSWLPAGCE 180
QY 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVLNKTILFSYGTNRNPEYIQLYL 240
DB 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVLNKTILFSYGTNRNPEYIQLYL 240
QY 241 SYQSIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300
DB 241 SYQSIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300
QY 301 IVPEGGTLOIGQKNGCCVGGGDETLAFSGRLTGNIWDSVLSNBEIRETGGAESCHIR 360
DB 301 IVPEGGTLOIGQKNGCCVGGGDETLAFSGRLTGNIWDSVLSNBEIRETGGAESCHIR 360
QY 361 GNIVGSGVTEIQPHGGAQYVS 381
DB 361 GNIVGSGVTEIQPHGGAQYVS 381

RESULT 2
PTX3_MOUSE
ID PTX3_MOUSE STANDARD; PRT; 381 AA.
AC P48759;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR-
INDUCIBLE PROTEIN TSG-14).
GN PTX3 OR TSG14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [?]

RP SEQUENCE FROM N.A.
RC STRAIN=C57; TISSUE=Fibroblast;
RX MEDLINE=96202510; PubMed=8634434;
RA Introna M., Vidal Alles V., Castellano M., Picardi G., de Gioia L.,
RA Bottezzati B., Peri G., Breviaro F., Salmons M., de Gregorio L.,
RA Dragani T.A., Srinivasan N., Blundell T.L., Hamilton T.A.,
RA Mantovani A.;
RT "Cloning of mouse ptx3, a new member of the pentraxin gene family
expressed at extrahepatic sites.";
RL Blood 87:1862-1872(1996).
RN [2]
RP SEQUENCE OF 1-177 FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96029644; PubMed=7592730;
RA Altmeyer A., Klampfer L., Goodman A.R., Vilcek J.;
RT "Promoter structure and transcriptional activation of the murine
TSG-14 gene encoding a tumor necrosis factor/interleukin-1-inducible
pentraxin protein.";
RL J. Biol. Chem. 270:25584-25590(1995).
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

EMBL; X83601; CAA58580.1; -;
EMBL; U33842; AAC52273.1; -;
MGD; MGI:104641; Ptx3.
InterPro; IPR001759; Pentaxin.
Pfam; PF00354; pentaxin; 1.
PRINTS; PR00895; PENTAXIN.
SMART; SM00159; PTX; 1.
PROSITE; PS00289; PENTAXIN; 1.
Pentaxin; Glycoprotein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 381 PENTAXIN-RELATED PROTEIN PTX3.
FT DOMAIN 183 381 PENTAXIN.
FT DISULFID 210 271 BY SIMILARITY.
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 50 50 R -> A (IN REF. 2).
FT CONFLICT 90 90 A -> S (IN REF. 2).
FT CONFLICT 161 161 A -> S (IN REF. 2).
FT CONFLICT 172 172 R -> H (IN REF. 2).
FT SEQUENCE 381 AA; 41811 MW; E3CA3B1D93CFE4EB CRC64;

Query Match 83.1%; Score 1667; DB 1; Length 381;
Best Local Similarity 82.2%; Pred. No. 6.5e-122;
Matches 313; Conservative 22; Mismatches 46; Indels 0; Gaps 0;

QY 1 MHLAIFCALWSAVLAENSDDDYDLMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
DB 1 MHLAIFCALWSAVVAETSDDYELMYVNLNDNEIDNGLHPTEDPTCDCCQEHSEWDKLF 60
QY 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAGAPAPARLTSALDEL 120
DB 61 IMLENSQMRMLLQATDDVLRGELQRLREELGRLAESLARPCAGAPADARLVRLEPL 120
QY 121 LOATRDAGRRLARMEGAEOPEAGRALAAVLEELRQTRADLHAYOGVAARSWLPAGCE 180
DB 121 LOESRDASLRLARLEDAEARRPEATVPGLGAVLEELRRLRADLSAVQSVARHWPAGCE 180
QY 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVLNKTILFSYGTNRNPEYIQLYL 240
DB 181 TAILFPMRSKKIFGSHVHPVRPMRLSFACIWKATDVLNKTILFSYGTNRNPEYIQLYL 240
QY 241 SYQSIVFVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300
DB 241 SSQSLVVLVVGGEENKLVAAEAMVSLGRWTHLCGTWNSEGLTSLWVNGELAATTVMATGH 300

```

QY 301 IYPEGILQIGKEKNGCCVGGGDETLAFSGRLTGFTNIWDSVLSNEEIRETGARSCHIR 360
DB 301 SVPEGLQIGKEKNGCCVGGGDESLAFSGRLTGFTNIWDRVLSNEEIRASGVESCHIR 360
QY 361 GNIVGWGVTEIOPHGAQYVS 381
DB 361 GNIVGWGVTEIOAHGAQYVS 381

RESULT 3
APEX_CAVPO STANDARD; PRT: 427 AA.
AC P47970;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE APEXIN PRECURSOR (ACROSOMAL PENTAXIN-LIKE PROTEIN P50) (AM50).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 223-227; 328-337 AND 342-377.
RC STRAIN-HARTLEY; TISSUE-Testis.
RX MEDLINE=95096119; PubMed=7798265;
RA Noland T.D., Friday B.B., Maulit M.T., Gerton G.L.;
RT "The sperm acrosomal matrix contains a novel member of the pentaxin
family of calcium-dependent binding proteins.";
RL J. Biol. Chem. 269:32607-32614(1994).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 254-279; 316-330 & 359-389.
RC STRAIN-HARTLEY; TISSUE-Testis.
RX MEDLINE=95096120; PubMed=7798266;
RA Reid M.S., Blobel C.P.;
RT "Apexin, an acrosomal pentaxin.";
RL J. Biol. Chem. 269:32615-32620(1994).
CC -1- FUNCTION: MAY BE INVOLVED IN BINDING, CONCENTRATING, AND SORTING
SOLUBLE GLYCOPROTEINS OR GLYCOLIPIDS THAT ARE DESTINED FOR THE
ACROSOME.
CC -1- SUBUNIT: OLIGOMERIC; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: SPERM ACROSOMAL MATRIX.
CC -1- TISSUE SPECIFICITY: TESTIS SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U13234; AAA64994.1; -.
CC EMBL: U13236; AAA64995.1; -.
CC HSP: P06205; LLIM.
CC InterPro: IPR001759; Pentaxin.
CC Pfam: PF00354; pentaxin; 1.
CC PRINTS: PR00895; PENTAXIN.
CC SMART: SM00159; PTX; 1.
CC PROSITE: PS00289; PENTAXIN; 1.
KW Pentaxin; Sperm; Glycoprotein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 427 APEXIN.
FT DOMAIN 223 427 PENTAXIN.
FT DISULFD 249 309 BY SIMILARITY.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 140 141 MISSING (IN REF. 2).
FT CONFLICT 279 279 E -> S (IN REF. 2; AA SEQUENCE).
FT CONFLICT 329 329 G -> S (IN REF. 2; AA SEQUENCE).
SQ SEQUENCE 427 AA; 47233 MW; D24F8F077A89E09A CRC64;

```

```

Query Match 14.8%; Score 296.5; DB 1; Length 427;
Best Local Similarity 24.5%; Pred. No. 1e-15;
Matches 94; Conservative 60; Mismatches 121; Indels 109; Gaps 14;

QY 67 QMRERMLQ-----ATDDVLRLGELORLREELG-----RLAESLA 100
DB 65 QLRETVVMQKETLGAQREAIRELTSKLARCEGLMAGKAESSKDTGDLPRDPSRVVEQLS 124
QY 101 RPCA-----PGAPAEAR--LTSALDELLOATRDAGRRLARME---- 135
DB 125 RSLQVLKDRLESLELQRLTNASNTGLPSPDFREVLRQLGEL---ERQLLRKVAELEDERS 181
QY 136 -----GAEAQRPPEAGRALAAVLELROTRADLHVAQVGAARSWLPACGTAILPEPMRS 189
DB 182 LLHNETSAAHQQTENTNALLQRTVTELERGNSAFKSPDAF-----KVSLLPFR 229
QY 190 KFIQSVHVPVRMRLESFSPACIVWKAT-----DVLNKTILFSYCTKENPYE 235
DB 230 NYLYGKIKKTLPL-ELYSFYICLWLKSSASPGIGTSPSYAVPGQANEIVLIEWG--NNPIE 286
QY 236 IQLYLSYSQISVFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSSEGLTSLWVNGELAAAT 293
DB 287 LLI-----NDKVAQLPLFVSDGKWHHCITWTTRDGLWEAFQDGEKLG 331
QY 294 VEMATGHIVPEGGILQIGKEKNGCCVGGGDETLAFSGRLTGFTNIWDSVLSNEEIRETG 353
DB 332 ENLAWHPRIKSGVLTILGOEQD--TVGGRFDATAOPVGLSOFNIWDRVLRQPEISNIAN 389
QY 354 AESCHIRGNIVGWVTEIOPHGA 377
DB 390 C-SLMAGNIIPWVDNNVDVFGGA 412

RESULT 4
NPX2_HUMAN
ID NPX2_HUMAN STANDARD; PRT: 430 AA.
AC P47972;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE NEURONAL PENTAXIN II PRECURSOR (NP-II) (NP2).
GN NPX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96015050; PubMed=8530029;
RA Hsu Y.-C., Perin M.S.;
RT "Human neuronal pentaxin II (NPX2): conservation, genomic
structure, and chromosomal localization.";
RL Genomics 28:220-227(1995).
CC -1- SUBCELLULAR LOCATION: SECRETORY VESICLES (POTENTIAL).
CC -1- TISSUE SPECIFICITY: BRAIN, PANCREAS, LIVER, HEART, AND SKELETAL
MUSCLE. HIGHEST LEVELS ARE SEEN IN THE TESTIS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U29195; AAA68980.2; -.
CC EMBL: U29191; AAA68980.2; JOINED.
CC EMBL: U29192; AAA68980.2; JOINED.
CC EMBL: U29193; AAA68980.2; JOINED.

```

THE NEURONAL AND GLIAL UPTAKE OF THE SNAKE VENOM TOXIN TAIPOXIN.

-1- SUBCELLULAR LOCATION: SECRETORY VESICLES (POTENTIAL).

-1- TISSUE SPECIFICITY: CEREBELLUM, HIPPOCAMPUS AND CEREBRAL CORTEX.

-1- PTM: GLYCOSYLATED.

-1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; U18772; AAA92685.1; --
HSP; P06205; 1LIM.
InterPro: IPR001759; Pentaxin.
Pfam: PF00354; pentaxin; 1.
PRINTS; PR00895; PENTAXIN.
SMART; SM00159; PTX; 1.
PROSITE; PS00289; PENTAXIN; 1.
Pentaxin; Signal; Glycoprotein.
SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 432 NEURONAL PENTAXIN I.
FT DOMA1N 230 432 PENTAXIN
FT DISULFID 256 316 BY SIMILARITY.
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 432 AA; 47216 MW; 3071E3E40ACA3820 CRC64;

QY 67 QMRERMLLQATDDVLURGE-LQRLREELGRLAESLARPCAPG----- 106

Db 60 QLR^{ET}VLQOKETILSQKETIRELT^{TT}KLGRCESQSTLDAGCEARSGGGRKOPGGKNTMG 119

QY 107 ---APAEARL-----TSAIDELIQAOTDACPBB--JA 132

```

db      || |
        ||| :||: | | :
120     PLSPBPASEPFI SOI GOMI OSI VTPI ENI FOVDFI NNOGCOMNUT KOTY SCUTS
        ++++++OATROBOKK --DA 132

```

0V -----ECAPMADDDNBNBNDP-----
133 BM-----ECAPMADDDNBNBNDP-----
136 BCBKRIINDBITCQUCQIQNGSUKIKLNDENDEQPSKNSSSQINSKLULLQSKLDLDERQVL5 I79

133 KM
EGALQRPPEAGRA - LAAVLEELRQTRADLHAVQGWAARSWLPAGCETAILFPM 187

DB 180 RVNTLEEGKGGPKNDTEERAKIESALTS LHQRISELEKGQ----KDRP-GDKFQLTFPL 234

QY 188 RSKKIFGSVHPVPRPMRLESFSACIWKATDV-----LNKTI LFSYGTGRNP 233

Db 235 RTNMYAKVKKSLP--EMYAF¹TCMWL²KSSA³APGV⁴GT⁵PF⁶SYAV⁷PGQAN⁸ELV⁹LI¹⁰EW¹¹--NNP 291

QY 234 YEIQLYLSYQSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTISLWVNGELAA^{TT} 293

```
db      || ;   : ||:          | : | : | : | : | : | : | : | : | : |
292 MEILINDKVAKLPEVIND-----GKWHHCVTWTRDGVWFAYODSTOGSNG 338
```

294 VEWATGHI VPEGG I O I G O E K N G C C V C C E D E N T I A E S C B P I T C E N I U D S C H I C H E R I E R M O C C 252

[illegible]

000 ENLAF INF INFGVLVGGQD--I LGGGF DAT QAF V GELAHFN I WDRKLT PGEVINLAT 396

354 AESCHIRNIVGWGVTEIQPHGGA 377

397 CSSKALSGNVIAWESQIEIFGGA 420

RESULT 6

STANDARD	NPV1	MOUSE	NPX1_MOUSE
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
18	18	18	18
19	19	19	19
20	20	20	20
21	21	21	21
22	22	22	22
23	23	23	23
24	24	24	24
25	25	25	25
26	26	26	26
27	27	27	27
28	28	28	28
29	29	29	29
30	30	30	30
31	31	31	31
32	32	32	32
33	33	33	33
34	34	34	34
35	35	35	35
36	36	36	36
37	37	37	37
38	38	38	38
39	39	39	39
40	40	40	40
41	41	41	41
42	42	42	42
43	43	43	43
44	44	44	44
45	45	45	45
46	46	46	46
47	47	47	47
48	48	48	48
49	49	49	49
50	50	50	50
51	51	51	51
52	52	52	52
53	53	53	53
54	54	54	54
55	55	55	55
56	56	56	56
57	57	57	57
58	58	58	58
59	59	59	59
60	60	60	60
61	61	61	61
62	62	62	62
63	63	63	63
64	64	64	64
65	65	65	65
66	66	66	66
67	67	67	67
68	68	68	68
69	69	69	69
70	70	70	70
71	71	71	71
72	72	72	72
73	73	73	73
74	74	74	74
75	75	75	75
76	76	76	76
77	77	77	77
78	78	78	78
79	79	79	79
80	80	80	80
81	81	81	81
82	82	82	82
83	83	83	83
84	84	84	84
85	85	85	85
86	86	86	86
87	87	87	87
88	88	88	88
89	89	89	89
90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

FILED	STANDARD;	PRT; 432 AA.
NEAT_MOUSE		
AC Q62443;		
07 2004 1007		

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)
DE NEURONAL PENTRAXIN I PRECURSOR (NP-I) (NP1)

GN NPTX1.


```
QY 188 RSKKIFGSHVPRMRLSFACIWKATDV-----LNKTLIFSCTKRNK 233
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 233 RTNYAKVKSLLP-EMVAFVCMWLKSSATPGVGTPEFSAVPGQANLVLIWGG--NNP 289
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 234 YEIQYLSVQSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSSEGLTSLWVNGELAATT 293
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 290 MELLINDKVKLPFFVIND-----GKWHICVTVTTRDGVWEAYQDGTQGGSG 336
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 294 VEMATGHVPEGGIILQIGOEKNGCCVGGFDETLAFSGRLTGFNWDSVLNNEETREGG 353
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 337 ENLAPYHPKPGVLVQGEQD--TLGGGFDATQAFVGLAHFNWDRKRLTPGVEYNLAT 394
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 354 AESCHIRGNVGVGTETQPHGGA 377
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 395 CSTKALSGNVIAWAEISHIEYVGA 418
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 8
CRP4_LIMPO STANDARD; PRT; 242 AA.
P06206;
01-JAN-1988 (Rel. 06, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
DE C-REACTIVE PROTEIN 1.4 PRECURSOR.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278105; PubMed=3015932;
RA Nguyen N.Y., Suzuki A., Cheng S.-M., Zon G., Liu T.-Y.;
RT "Isolation and characterization of Limulus C-reactive protein genes.";
RL J. Biol. Chem. 261:10450-10455(1986).
RN [2]
RP SEQUENCE OF 25-242, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=86278106; PubMed=2426265;
RA Nguyen N.Y., Suzuki A., Boykins R.A., Liu T.-Y.;
RT "The amino acid sequence of Limulus C-reactive protein. Evidence of
polymorphism.";
RL J. Biol. Chem. 261:10456-10465(1986).
CC -!- FUNCTION: MIGHT SERVE THE ROLE OF IMMUNOGLOBULINS.
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
CC EMBL; M14024; AAA28268.1;
CC PIR; A25192; A25192.
CC PIR; A25193; A25193.
CC HSP; P06205; ILM.
CC InterPro; IPR001759; Pentaxin.
CC Pfam; PF00354; Pentaxin.
CC PRINTS; PR00895; PENTAXIN.
CC SMART; SM00159; PTX, 1.
CC PROSITE; PS00289; PENTAXIN; 1.
CC Pentaxin; Calcium; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 242 C-REACTIVE PROTEIN 1.4.
FT DOMAIN 25 242 PENTAXIN.
FT DISULFID 62 125
FT DISULFID 112 144
FT DISULFID 207 241
FT CARBOHYD 147 147
FT DOMAIN 52 67 N-LINKED (GLCNAC...).
BINDING OF PHOSPHORYLCHOLINE (POTENTIAL).
```

```
FT DOMAIN 59 60 INTERACTION WITH PHOSPHATE GROUP OF
FT BINDING 63 63 PHOSPHORYLCHOLINE (POTENTIAL).
FT QUATERNARY AMMONIUM GROUP OF
FT PHOSPHORYLCHOLINE (POTENTIAL).
SQ SIMILAR 139 153 STRONG WITH CA-BINDING EF-HAND SEQUENCE.
SQ SEQUENCE 242 AA; 26842 MW; 8EC7AC5B47E76459 CRC64;

Query Match 12.8%; Score 256.5; DB 1; Length 242;
Best local similarity 29.4%; Pred. No. 6.3e-13;
Matches 60; Conservative 42; Mismatches 87; Indels 15; Gaps 6;

QY 183 ILFPMRSKIFGSHVPRM-RLESEFACIWKATDVLNKTLIFSCTKRNKPYEIQYLS 241
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 34 VKFPPSSPFPRLVMVGTLPDQETLCYFWKVNHLKSTLTIFSYTAKNDNELLTSLE 93
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 242 YQSI--VFVVGGEENKLVAEAMVSLGRWTHLCGTWNSSEGLTSLWVNG-ELAATTVMAT 298
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 94 KQGAHNMVHGAPOLKVQCPNKTHIGKWHVHCHTWSSWEGEATIGVDGPHCKGNATGAM 153
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 299 GHIVPEGGIILQIGOEKNGCCVGGFDETLAFSGRLTGFNWDSVLNNEETREGGAES- 357
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 154 GVTLSQGLVVLQGEQDS--VGGEYDAEQSLEGESELNLTWNTVNLNHEQIKH---LSKCA 208
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 358 -----HIRGNIVGVGTETQPHGG 376
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 209 HPSERHIFGNIIQWDKTFQAYDG 232
|: : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 9
CRP3_LIMPO STANDARD; PRT; 242 AA.
AC P06207;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
DE C-REACTIVE PROTEIN 3.3 PRECURSOR.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278105; PubMed=3015932;
RA Nguyen N.Y., Suzuki A., Cheng S.-M., Zon G., Liu T.-Y.;
RT "Isolation and characterization of Limulus C-reactive protein genes.";
RL J. Biol. Chem. 261:10450-10455(1986).
RN [2]
RP SEQUENCE OF 25-242, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=86278106; PubMed=2426265;
RA Nguyen N.Y., Suzuki A., Boykins R.A., Liu T.-Y.;
RT "The amino acid sequence of Limulus C-reactive protein. Evidence of
polymorphism.";
RL J. Biol. Chem. 261:10456-10465(1986).
CC -!- FUNCTION: MIGHT SERVE THE ROLE OF IMMUNOGLOBULINS.
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
CC EMBL; M14025; AAA28269.1;
CC PIR; B25192; B25192.
CC PIR; B25193; B25193.
CC HSP; P06205; ILM.
CC InterPro; IPR001759; Pentaxin.
CC Pfam; PF00354; Pentaxin.
CC PRINTS; PR00895; PENTAXIN.
CC SMART; SM00159; PTX, 1.
CC PROSITE; PS00289; PENTAXIN; 1.
CC Pentaxin; Calcium; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 242 C-REACTIVE PROTEIN 1.4.
FT DOMAIN 25 242 PENTAXIN.
FT DISULFID 62 125
FT DISULFID 112 144
FT DISULFID 207 241
FT CARBOHYD 147 147
FT DOMAIN 52 67 N-LINKED (GLCNAC...).
BINDING OF PHOSPHORYLCHOLINE (POTENTIAL).
```

```
DR PRINTS: PRO0895; PENTAXIN.
DR SMART: SM00159; PTX; 1.
DR PROSITE: PS00289; PENTAXIN; 1.
KW Pentaxin; Calcium; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 242 C-REACTIVE PROTEIN 3.3.
FT DOMAIN 25 242 PENTAXIN.
FT DISULFID 62 125
FT DISULFID 112 144
FT DISULFID 207 241
FT CARBOHYD 147 147
FT DOMAIN 52 67
FT DOMAIN 59 60
FT BINDING 63 63
FT SIMILAR 139 153
FT SEQUENCE 242 AA; 26720 MW; C45E47EF54B8C869 CRC64;

Query Match 12.4%; Score 249.5; DB 1; Length 242;
Best Local Similarity 28.9%; Pred. No. 2.2e-12;
Matches 58; Conservative 43; Mismatches 91; Indels 9; Gaps 5;

QY 183 ILFPMRSKIFGSHVPRPM-RLEFSACIWKATDVLNKTLFSGYTKRNPYEIQLYLS 241
Db 34 VKPPSSPSFPLVMVGLPDLQETILCYWFKVNLKGLTHMFSYATAKKNELLTLD 93
QY 242 YQS--IVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSSEGLTSLWNG-ELAATTVMAT 298
Db 94 EQGDFLNVHGAPOQLKVCQPNKIHGKWHVCHTWSWGEATVADGPHCKGNATGIAV 153
QY 299 GHIVPEGILQIGQKNGCCVGGFDETLAFSGRLTGFINWDSVLSNEEIR---ETGGAE 355
Db 154 GRTLQGLVGLQDQDS--VGKFDATQSLGELSELNLNVTNLNHEQIKYLSKCAHPS 211
QY 356 SCHIRGNIVGWVTEIOPHGG 376
Db 212 ERHIYGNIIQWDKTPKAYDG 232

RESULT 10
CRP1_LIMPO STANDARD; PRT; 242 AA.
AC P06205;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
C-REACTIVE PROTEIN 1.1 PRECURSOR.
Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
NCBI_TaxID=6850;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86278105; PubMed=3015932;
RA Nguyen N.Y., Suzuki A., Cheng S.-M., Zon G., Liu T.-Y.;
RT "Isolation and characterization of Limulus C-reactive protein genes.";
RL J. Biol. Chem. 261:10450-10455(1986).
[2]
RN SEQUENCE OF 25-242, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=86278106; PubMed=2426265;
RA Nguyen N.Y., Suzuki A., Boykins R.A., Liu T.-Y.;
RT "The amino acid sequence of Limulus C-reactive protein. Evidence of
polymorphism.";
RL J. Biol. Chem. 261:10456-10465(1986).
[3]
RN 3D-STRUCTURE MODELING.
RX MEDLINE=95187705; PubMed=7881902;
RA Srinivasan N., White H.E., Emsley J., Wood S.P., Pepys M.B.,
RA Blundell T.L.;
RT "Comparative analyses of pentraxins: implications for protomer
assembly and ligand binding.";
```



```
ID * CRP_MESAU STANDARD: PRT: 225 AA.
AC P49262;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE C-REACTIVE PROTEIN PRECURSOR.
GN PTX1 OR CRP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91369977; PubMed=1892852;
RA Dowton S.B., Holden S.N.;
RT "C-reactive protein (CRP) of the Syrian hamster.";
RL Biochemistry 30:9531-9538(1991).
CC -!- FUNCTION: CRP DISPLAYS SEVERAL FUNCTIONS ASSOCIATED WITH HOST
CC PHAGOCYTOSIS, & COMPLEMENT FIXATION THROUGH ITS CALCIUM-DEPENDENT
CC BINDING TO PHOSPHORYLCHOLINE (BY SIMILARITY).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- INDUCTION: BY INTERLEUKIN 1, INTERLEUKIN 6, AND TUMOR NECROSIS
CC FACTOR.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S56005; AAB19893.2; -
DR HSP; P02741; LGNH.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
KW Acute phase; Plasma; Calcium; Pentaxin; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 225 C-REACTIVE PROTEIN.
FT DOMAIN 20 225 PENTAXIN.
FT DISULFID 55 116 BY SIMILARITY.
FT SEQUENCE 225 AA; 24822 MW; 00B439C45D58E05A CRC64;
-----
Query Match 10.8%; Score 217.5; DB 1; Length 225;
Best Local Similarity 28.5%; Pred. No. 6e-10;
Matches 57; Conservative 38; Mismatches 92; Indels 13; Gaps 7;
QY 180 ETAILFPMSKKTGSGVHPVRPRLSFSACTIWW-KATDVLNKTILFSYGTARNYEIQL 238
DB 25 KTAFFPKESANSYVSLQAQSKTKTKAFTVCLHITELSTTRSFISYATKNSPNEILI 84
QY 239 YLSY-QSTVFVVGGENKLVAEMVSLGRWTHLCGTWNSEGLTSLWVNGELAAATTVEA 297
DB 85 FMSKRGVAFVGGGPEVLFKASEIEVP--THICASWESATGIAELWDGKPKVKI-LQ 141
QY 298 TGHIVPEGGIILQIQEKNGCCVGGGDETAFSGRLTGFNIWDSVLSNBEIRE--TGGAE 355
DB 142 KGYTVGTDAIILGQEQDS--YGGGFDANOSLVGDIGVNMWDIVLSPEQINTVCVGGT- 198
QY 356 SCHIRGNIVGWGVTEIQPHG 375
DB 199 ---LDPSVLNMQALKYKVGQ 215
RESULT 14
```

```
FP_CRIMI STANDARD: PRT: 231 AA.
ID FP_CRIMI
AC P15697;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FEMALE PROTEIN PRECURSOR (FP) (SERUM AMYLOID P-COMPONENT).
OS Cricetus migratorius (Armenian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10032;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90063074; PubMed=2479691;
RA Dowton S.B., Waggoner D.J.;
RT "Armenian hamster female protein (serum amyloid P component).
RT Comparison with the sex-regulated homolog in Syrian hamster.";
RL J. Immunol. 143:3776-3780(1989).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- MISCELLANEOUS: PLASMA CONCENTRATION OF FP ARE ALTERED BY SEX
CC STEROIDS AND BY STIMULI THAT ELICIT AN ACUTE PHASE RESPONSE.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY. ORTHOLOG OF HUMAN SAP.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31610; AAA36981.1; -
DR PIR; A45814; A45814.
DR HSP; P07629; LHAS.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
KW Pentaxin; Plasma; Acute phase; Calcium; Signal.
FT SIGNAL 1 19 FEMALE PROTEIN.
FT CHAIN 20 231 PENTAXIN.
FT DOMAIN 20 231 BY SIMILARITY.
FT DISULFID 55 114 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 51 51
FT SEQUENCE 231 AA; 26353 MW; A4D12A9DDE70B823 CRC64;
-----
Query Match 10.6%; Score 212.5; DB 1; Length 231;
Best Local Similarity 28.7%; Pred. No. 1.5e-09;
Matches 58; Conservative 33; Mismatches 88; Indels 23; Gaps 6;
QY 184 LFPMSKKTGSGVHPVRPRLSFSACTIWW-KATDVLNKTILFSYGTARNYEIQLY---- 239
DB 29 VPPRESSEYVVLIPRLKPLENFTLC-FRTYDLSRPHSLFSYNKNDNELLIKERM 87
QY 240 ----LSYQSIIVFVVGGENKLVAEMVSLGRWTHLCGTWNSEGLTSLWVNGELAAATTVE 295
DB 88 GEYGLYIENLGAIVRGVE-----EFASPVHFTCSWESSGIAEFVWG-IPVWKG 137
QY 296 MATGHIVPEGGIILQIQEKNGCCVGGGDETAFSGRLTGFNIWDSVLSNBEIRETGGAE 355
DB 138 LKKGYTVKTPQSTIILGQEQDN--YGGGFDKQSGFVGMGDLNMDVSLTPPEIKSV--YE 193
QY 356 SCHIRGNIVGWGVTEIQPHGGA 377
DB 194 GSWLEANILDWRTLNYEMSGYA 215
RESULT 15
CRP_MOUSE
```

[illegible]

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:21 ; Search time 31.68 Seconds
(without alignments)
1759.146 Million cell updates/sec

Title: US-09-555-473-1
Perfect score: 2007
Sequence: 1 MHLAIFCALMSAVLAENS.....NIVGWGVTETQPHGGAQYVS 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: . 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.17.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	14.7	429	11 070340	070340 mus musculus
2	293	14.6	494	11 035764	035764 rattus norv
3	289.5	14.4	432	11 P97738	P97738 rattus norv
4	280.5	14.0	202	5 Q98Y6	Q98Y6 tachyples
5	278	13.9	499	4 Q95502	Q95502 homo sapien
6	268.5	13.4	493	11 Q99J85	Q99J85 mus musculus
7	259.5	12.9	202	5 Q98Y8	Q98Y8 tachyples
8	259.5	12.9	202	5 Q98Y7	Q98Y7 tachyples
9	253.5	12.6	202	5 Q98Z4	Q98Z4 tachyples
10	249.5	12.4	202	5 Q98Z6	Q98Z6 tachyples
11	248.5	12.4	202	5 Q98Z9	Q98Z9 tachyples
12	247.5	12.3	202	5 Q9900	Q9900 tachyples
13	247.5	12.3	202	5 Q98Z8	Q98Z8 tachyples
14	246.5	12.3	202	5 Q98Z1	Q98Z1 tachyples
15	246.5	12.3	202	5 Q98Y9	Q98Y9 tachyples
16	245.5	12.2	202	5 Q98Z5	Q98Z5 tachyples
17	245.5	12.2	202	5 Q98Z0	Q98Z0 tachyples
18	242.5	12.1	202	5 Q98Z2	Q98Z2 tachyples
19	240.5	12.0	202	5 Q98Z7	Q98Z7 tachyples

20	229.5	11.4	3567	11 Q9ES77	Q9es77 mus musculus
21	228.5	11.4	202	5 Q98Y1	Q98y1 tachyples
22	228.5	11.4	202	5 Q98Y0	Q98y0 tachyples
23	225.5	11.2	240	11 Q9D1A3	Q9d1a3 mus musculus
24	224.5	11.2	202	5 Q98X9	Q98x9 tachyples
25	219.5	10.9	202	5 Q98Z3	Q98z3 tachyples
26	213.5	10.6	202	5 Q98Y5	Q98y5 tachyples
27	213.5	10.6	202	5 Q98Y3	Q98y3 tachyples
28	212.5	10.6	202	5 Q98Y4	Q98y4 tachyples
29	211.5	10.5	223	11 Q63913	Q63913 cricetus
30	205.5	10.2	202	5 Q98Y2	Q98y2 tachyples
31	197.5	9.8	219	11 Q9D8J8	Q9d8j8 mus musculus
32	190	9.5	225	13 Q9PTT2	Q9ptt2 lepidobatra
33	187	9.3	222	6 Q19062	Q19062 sus scrofa
34	176	8.8	236	13 P79905	P79905 salmo salar
35	166.5	8.3	200	11 Q9D8V2	Q9d8v2 mus musculus
36	165	8.2	236	13 P79899	P79899 oncorhynch
37	155.5	7.7	224	6 Q19063	Q19063 sus scrofa
38	138	6.9	606	2 Q86584	Q86584 streptomyce
39	135.5	6.8	558	5 Q76933	Q76933 drosophila
40	135.5	6.8	558	5 Q9V3N9	Q9v3n9 drosophila
41	119.5	6.0	1627	4 Q13219	Q13219 homo sapien
42	117	5.8	1503	2 Q52973	Q52973 bacillus ci
43	115	5.7	4199	2 P74440	P74440 synecocyst
44	114	5.7	521	4 Q9Y5J1	Q9y5j1 homo sapien
45	112	5.6	1000	5 Q9NKG8	Q9nkg8 leishmania

ALIGNMENTS

RESULT 1
O70340
ID O70340; PRELIMINARY; PRT; 429 AA.
AC O70340;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE NEURONAL PENTRAXIN 2.
GN NPTX2 OR NP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Perin M.S.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Perin M.S.;
RT "Mouse neuronal pentraxin 2 gene.";
DR EMBL; AF049124; AAC05131.1; -;
DR EMBL; AF318618; AAK06745.1; -;
DR HSSP; P06205; LLIN.
DR MGD; MGI:1858209; Nptx2.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00389; PENTAXIN; 1.
SQ SEQUENCE . 429 AA; 47136 MW; 638EED14C4CECA28 CRC64;

Query Match 14.7%; Score 295; DB 11; Length 429;

Best Local Similarity 25.5%; Pred. No. 4.1e-15;

Matches 98; Conservative 56; Mismatches 122; Indels 108; Gaps 14;

QY 67 QMRMLLQATDDVLRLGELQRLRELGRLA--ESLA-----RCPACAPAE 110

DB 66 QLRRTVVQQ--KETLGAQREAIKELTGKLRCEGLAGGARGTKMGDLPDPGHVVE 123

```
QY 111 -----ARLTSALDELLO-----ATRDAGRRLARME----- 135
DB 124 QLSRSLQTLKDRLESLQLQRTVNSNAGLSPDFREVLQRLGELERQLLRKVAELEDEKS 183
QY 136 -----GAEARPEEAGRAALAELEELQRTADLHAYOGVWAARSWLPAGCETAILFPMS 189
DB 184 LLHNETSARHQKTESTLNALLQRLVTELEGRNSAFKSPDAF-----KVSPLPRT 231
QY 190 KKFSGVHPVRPMRLESFSAIWKAT-----DVLNKTILFSYGTGRNPE 235
DB 232 NYLGGKIKKLP-ELYAFTICLWRSSASPGIGTPFSYAVPGQANEIVLIENG--NNPIE 288
QY 236 IQLYLSYQSIVFVVGGENKLVAE--AMVSLGRWTHLCGTWNSBEGLTSLWVNGELAATT 293
DB 289 LLI-----NDKVAQLPLFVSDGKWHHCITWTRDGMWEAFQDGEKLG 333
QY 294 VEMATGHIVPEGGLIQGKNGCCVGGFDETLAFSGRLTGNNWDSVLSNEIRETGG 353
DB 334 ENLAPWPIKPGVLLILGQEQD--TVGGRFDATQAFVGEISQFNMDRVLRAQEIINIAN 391
QY 354 AESCHIRGNIVGWGVTEIQPHGGA 377
DB 392 C-STNMPGNIIPWVDNNDVFEVGA 414

RESULT 2
ID 035764 PRELIMINARY; PRT; 494 AA.
AC 035764;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE NEURONAL PENTRAXIN RECEPTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RA Dadds D.C., Omeis I.A., Cushman S.J., Helms J.A., Perin M.S.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005099; AAB62885.1;
DR HSSP; P02743; ISAC.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF003354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
R SEQUENCE 494 AA; 52370 MW; FEC996CA311E40E2 CRC64;
Q

Query Match 14.6%; Score 293; DB 11; Length 494;
Best Local Similarity 28.2%; Pred. No. 7.1e-15;
Matches 98; Conservative 58; Mismatches 123; Indels 68; Gaps 17;

QY 56 WDK--LFIMLENSQMRMLQATDDVLRELQRLREEL---GRLESLARPCAPGAPAE 110
DB 179 WSPALLVELENVR-----ALDRIERIEQELPARGNLSSAPAPAVPTA--- 224
QY 111 ARLTSALDELLOATDRGRRLARMEGAEARPEEAGRAALAELEELQRTADLHAYOGV 169
DB 225 --LHSMDEL-----EGOLLAKVLALEKER-----AALSHGSHQORQEVEKELDALQGR 271
QY 170 AARSWLPAGCET-----AILEPMRSKKIFGSHVHPVRPMRLESFSAIWKATDVLNKT 222
DB 272 VAE--LEHGSSAYSPDPAFKVSIPIRNMYARVRAVP-ELYAFTACMWLRSR----- 322
QY 223 ILFSYGT-KNPVEIQIYLSYQSIVFVGEE-----NKLVAEMVSL--GRWTHLCGT 273
DB 323 ---SGSGGQTPFSYVPGQANEIVLIENGAGLEPMELLINDKVAQLPLSLKSDSNWHHCIA 379
QY 333 ENLAPWPIKPGVLLILGQEQD--TVGGRFDATQAFVGEISQFNMDRVLRAQEIINIAN 391
DB 392 C-STNMPGNIIPWVDNNDVFEVGA 414
```

```
DB 380 WTRDGLWSAYQDELRGSGENLAAWHPKIPGHGILLIGQEQD--TLGGRFDATQAFVGD 437
QY 334 TGNWDSVLSNEIRETGAESC--HIRGNIVGWGVTEIQPHGGAQ 378
DB 438 AQNLMDHALTPAQLV---GIANCTGPMGNVLPWEDKLVEAFEGGAK 481

RESULT 3
ID P97738 PRELIMINARY; PRT; 432 AA.
AC P97738;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE NARP.
CN NARP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=96256683; PubMed=8786423;
RA Tsui C.C., Copeland N.G., Gilbert D.J., Jenkins N.A., Barnes C.,
RA Worley P.F.;
RT "Narp, a novel member of the pentraxin family, promotes neurite
RT outgrowth and is dynamically regulated by neuronal activity.";
RL J. Neurosci. 16:2463-2478(1996).
DR EMBL; S82649; AAB46783.1;
DR HSSP; P06205; ILIM.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF003354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
R SEQUENCE 432 AA; 47429 MW; DD642A6AA323D24A CRC64;
Q

Query Match 14.4%; Score 289.5; DB 11; Length 432;
Best Local Similarity 27.4%; Pred. No. 1.1e-14;
Matches 90; Conservative 51; Mismatches 118; Indels 69; Gaps 12;

QY 81 LRGELORLREELGRLESLARPCAPGAPARLTSALDELLO-----ATRDAGRRLARME 135
DB 128 LRSRLQTLKDRL---ESLEQLQHTNA-SNAGLSPDFREVLQRLGELERQLLRKVAELE 182
QY 136 -----GAEARPEEAGRAALAELEELQRTADLHAYOGVWAARSWLPAGCETAILF 185
DB 183 DEKSLHNETSARHQKTESTLNALLQRLVTELEGRNSAFKSPDAF-----KVS 230
QY 186 PMRSKKIFGSHVHPVRPMRLESFSAIWKAT-----DVLNKTILFSYGTGR 231
DB 231 PLRTNLYGKIKKTLF-ELYAFTICLWRSSASPGIGTPFSYAVPGQANEIVLIENG--N 287
QY 232 NPVEIQIYLSYQSIVFVVGGENKLVAE--AMVSLGRWTHLCGTWNSBEGLTSLWVNGEL 289
DB 288 NPTELLI-----NDKVAQLPLFVSDGKWHHCITWTRDGMWEAFQDGEK 332
QY 290 AATVTVMATGHIVPEGGLIQGKNGCCVGGFDETLAFSGRLTGNNWDSVLSNEEIR 349
DB 333 LGTGENLAPWPIKPGVLLILGQEQD--TVGGRFDATQAFVGEISQFNMDRVLRAQEI 390
QY 350 ETGGAESCHIRGNIVGWGVTEIQPHGGA 377
DB 391 NIANC-STNMPGNIIPWVDNNDVFEVGA 417

RESULT 4
ID Q08Y6 PRELIMINARY; PRT; 202 AA.
AC Q08Y6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
```

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:21 ; Search time 21.12 Seconds
(without alignments)
1374.172 Million cell updates/sec

Title: us-09-555-473-1

Perfect score: 2007

Sequence: 1 MLLAILFCAWSAVLAENS.....NIVGWSVTEIQPHGAQYVS 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: -219241 seqs, 76174552 residues

i number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2007	100.0	381	2	A44323
2	296.5	14.8	427	2	A55496
3	289.5	14.4	432	2	T10894
4	256.5	12.8	242	2	A25192
5	253.5	12.6	218	2	C25193
6	252.5	12.6	218	2	B25193
7	249.5	12.4	242	2	B25192
8	248.5	12.4	242	2	C25192
9	225.5	11.2	230	2	A42579
10	217.5	10.9	225	2	A40326
11	212.5	10.6	231	2	A45814
12	211.5	10.5	223	2	I59479
13	203.5	10.1	225	2	A31563
14	200.5	10.0	225	1	CJRB
15	192.5	9.6	211	2	A4177
16	192.5	9.6	225	2	JX0259
17	187.5	9.3	234	2	A48593
18	184.5	9.2	224	1	CJHU
19	183.5	9.1	228	2	S11473
20	181	9.0	238	2	A45487
21	165	8.2	224	2	A30528
22	164.5	8.2	223	2	JX0260
23	161.5	8.0	223	1	YLHUP
24	138	6.9	606	2	T37217
25	119.5	6.0	1627	2	S65464
26	117	5.8	1503	2	T18266
27	115	5.7	4199	2	S76412
28	112.5	5.6	899	2	S12319
29	110	5.5	472	2	G83335

30 106 5.3 320 2 T08493 probable regulator
31 106 5.3 472 2 T30831 hypothetical prote
32 99 4.9 304 2 JX0209 lectin, galactose/
33 98.5 4.9 2101 2 A42184 nuclear mitotic ap
34 97.5 4.9 856 2 E75292 GDEF family prote
35 97 4.8 775 2 B82671 general secretory
36 97 4.8 1170 2 A57650 repair protein XPG
37 96.5 4.8 774 2 D83208 probable ferredoxi
38 95.5 4.8 316 2 JC6549 apolipoprotein E p
39 95.5 4.8 3972 2 S75251 hypothetical prote
40 95 4.7 284 2 A33085 tropomyosin - bloo
41 95 4.7 3063 2 S55505 fatty-acid synthas
42 95 4.7 10223 2 T30225 polyketide synthas
43 94 4.7 527 1 S25478 heat shock transcr
44 92 4.6 306 2 A42230 lectin M-ASGP-BP p
45 92 4.6 400 2 T46526 probable hydroxyly

ALIGNMENTS

RESULT 1

A44323

pentaxin PTX3 precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Jun-1993 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999

C:Accession: A44323; S18947; S17069; S37597

R:Breviaro, F.; d'Aniello, E.M.; Golay, J.; Peri, G.; Bottazzi, B.; Bairoch, A.; Sac

J. Biol. Chem. 267, 22190-22197, 1992

A:Title: Interleukin-1-inducible genes in endothelial cells. Cloning of a new gene re

A:Reference number: A44323; MUID:93054498

A:Accession: A44323

A:Molecule type: mRNA

A:Residues: 1-47, 'A', 49-381 <BR1>

A:Experimental source: umbilical vein endothelial cells

R:Breviaro, F.; d'Aniello, E.M.; Golay, J.; Bairoch, A.; Dejana, E.; Mantovani, A.;

submitted to the EMBL Data Library, January 1992

A:Description: Cloning of a new member of the pentaxin gene family from interleukin-1

A:Reference number: S18947

A:Accession: S18947

A:Molecule type: mRNA

A:Residues: 1-381 <BR2>

A:Cross-references: EMBL:X63613; NID:g35796; PIDN:CAA45158.1; PID:g35797

C:Genetics:

A:Gene: GDB:PTX3

A:Cross-references: GDB:I36459

A:Map position: 3q25-3q25

F:1-17/Domain: signal sequence #status predicted <SIG>

Query Match 100.0%; Score 2007; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.8e-151;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLAILFCAWSAVLAENSDDYDLMYVNLNDINGLHPTEDPTPCDGGHSEWDLKF 60

Db 1 MLLAILFCAWSAVLAENSDDYDLMYVNLNDINGLHPTEDPTPCDGGHSEWDLKF 60

Qy 61 IMLENSOMRERMLQATDDVLRGELQRLREELGRLAESLARPCAPAPAEARLTSSALDEL 120

Db 61 IMLENSOMRERMLQATDDVLRGELQRLREELGRLAESLARPCAPAPAEARLTSSALDEL 120

Qy 121 LQATRDAGRRLARMEGAQRPPEAGRALAAVLEELRQTRADLHAVQGWAAARSWLPACGE 180

Db 121 LQATRDAGRRLARMEGAQRPPEAGRALAAVLEELRQTRADLHAVQGWAAARSWLPACGE 180

Qy 181 TAILFPMSKSKIFGSHVHPVRPMRLSFSACTIVKATDVLNKTILFSYCTKRNPIQLYL 240

Db 181 TAILFPMSKSKIFGSHVHPVRPMRLSFSACTIVKATDVLNKTILFSYCTKRNPIQLYL 240

Qy 241 SYQSIVFVVGGEENKLVAAEMVSLGRWTHLCGTWNSBGLTSLWVNGELAAATTVMATGH 300

|||||

Db 241 STQSTVFVVVGGENKLVAEMVSLGRWTHLCGTWNSRGLTSLVWNGELAAATVEMATCH 300
QY 301 IVEGGIILQIGKKNCCVGGGDFETLAFSGRLTGFTNWDVSLNNEEIRETGAESCHIR 360
Db 301 IVEGGIILQIGKKNCCVGGGDFETLAFSGRLTGFTNWDVSLNNEEIRETGAESCHIR 360
QY 361 GNIVGWVTEIQPHGGAQYVS 381
Db 361 GNIVGWVTEIQPHGGAQYVS 381
RESULT 2
A55496
apexin precursor - guinea pig
N:Alternate names: 50K pentaxin, acrosomal
C:Species: Cavia porcellus (guinea pig)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55496; A55497
R:Noland, T.D.; Friday, B.B.; Maulit, M.T.; Gerton, G.L.
J. Biol. Chem. 269, 32607-32614, 1994
Title: The sperm acrosomal matrix contains a novel member of the pentaxin family of ca
Reference number: A55496; MUID:95096119
A:Accession: A55496
A:Molecule type: mRNA
A:Residues: 1-427 <NOI>
A:Cross-references: GB:U13234; NID:g595676; PIDN:AAA64994.1; PID:g595677
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Reid, M.S.; Blobel, C.P.
J. Biol. Chem. 269, 32615-32620, 1994
A:Title: Apexin, an acrosomal pentaxin.
A:Reference number: A55497; MUID:95096120
A:Accession: A55497
A:Molecule type: mRNA
A:Residues: 1-139,142-427 <REI>
A:Cross-references: GB:U13236; NID:g595678; PIDN:AAA64995.1; PID:g595679
A:Note: parts of this sequence were confirmed by peptide sequencing
C:Keywords: glycoprotein; sperm
F:144,185,389/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.8%; Score 296.5; DB 2: Length 427;
Best Local Similarity 24.5%; Pred. No. 9.2e-16;
Matches 94; Conservative 60; Mismatches 121; Indels 109; Gaps 14;
QY 67 QMRERMLQ-----ATDDVLRGELQRLREELG-----RLAESLA 100
Db 65 QURETWVWQKETLGAQREARELTSKLARCEGLMAGKAESSKDTMGDLPRDPSRVVEOLS 124
101 RPCA-----PCAPAEAR--LTSALDELLOATRDAGRRLARME---- 135
Db 125 RSLQVLKDRLESLEQLRTNASNTGLPSDFREVLQRLRGEL---ERQLLRKVAELEDKES 181
QY 136 -----GAEAPPEAGRALAAVLEELQTRADLHAGVQWAARSWLPAGCETAILFPMS 189
Db 182 LHNHETSAAHQKTENTLNAQLQVTELEGRNSAFKSPDAF-----KVSLPRT 229
QY 190 KKFSGVHPVRPMRLESFSAIWKAT-----DVLNKTILFSYGTGRNPE 235
Db 230 NYLYGKIKKTLF-ELYFTICLWLKSSASPGIGTFPSYAVPQCAINEIWLWG--NNPIE 286
QY 236 IQLYLSYSQSVFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSRGLTSLVWNGELAAIT 293
Db 287 LLI-----NDKVAQLPLFVSDGKWHHCITWTTRDGLWEAFQDGEKLG 331
QY 294 VEMATGHIVPEGGIILQIGKKNCCVGGGDFETLAFSGRLTGFTNWDVSLNNEEIRETGG 353
Db 332 ENLAPWHPIKSGVLLILGQEQD--TVGGRFDATQAFVGLSOFNIDRWLRVLPQELSNIAN 389
QY 354 AESCHIRGNIVGWVTEIQPHGGA 377
Db 390 C-SLNAGNIIPWVDNNDVDFGGA 412

RESULT 3
TI0894
neuronal pentraxin - rat
C:Species: Rattus sp. (rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: TI0894
R:Tsuji, C.C.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barnes, C.; Worley, P.F.
J. Neurosci. 16, 2463-2478, 1996
A:Title: Narp, a novel member of the pentraxin family, promotes neurite outgrowth and
A:Reference number: 217203; MUID:96256683
A:Accession: TI0894
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <TSU>
A:Cross-references: EMBL:S82649; NID:gl835928; PIDN:AA846783.1; PID:gl835929
C:Genetics:
A:Gene: Narp
C:Function:
A:Description: has lectin and growth-promoting activities
C:Keywords: pentraxin
Query Match 14.4%; Score 289.5; DB 2: Length 432;
Best Local Similarity 27.4%; Pred. No. 3.3e-15;
Matches 90; Conservative 51; Mismatches 118; Indels 69; Gaps 12;
QY 81 LRGELOLRREELGRLESLARPCAPAEARLTSALDELLO-----ATRDAGRRLARME 135
Db 128 LRSRLOTILKDL-----ESLEQLQHTNA-SNAGLPDFREVLQRLRGELERQLLRKVAELE 182
QY 136 -----GAEAPPEAGRALAAVLEELQTRADLHAGVQWAARSWLPAGCETAILF 185
Db 183 DEKSLHNHETSAAHQKTENTLNAQLQVTELEGRNSAFKSPDAF--KVSL 230
QY 186 PMRSKKIFGSHVPMRLESFSAIWKAT-----DVLNKTILFSYGTGR 231
Db 231 PLRTNYLYGKIKKTLF-ELYFTICLWLKSSASPGIGTFPSYAVPQCAINEIWLWG--N 287
QY 232 NPYETQLYLSYSQSVFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSRGLTSLVWNGEL 289
Db 288 NPIELLI-----NDKVAQLPLFVSDGKWHHCITWTTRDGLWEAFQDGEK 332
QY 290 AATVEMATGHIVPEGGIILQIGKKNCCVGGGDFETLAFSGRLTGFTNWDVSLNNEEIR 349
Db 333 LGTGENLAPWHPIKSGVLLILGQEQD--TVGGRFDATQAFVGLSOFNIDRWLRVLAQEI 390
QY 350 ETGGAESCHIRGNIVGWVTEIQPHGGA 377
Db 391 NIANC-STNMPGNIIPWVDNNDVDFGGA 417
RESULT 4
A25192
C-reactive protein chain 1.4 precursor - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 30-Jun-1988 #sequence_revision 31-Dec-1988 #text_change 20-Aug-1999
C:Accession: A25192; A25193
R:Nguyen, N.Y.; Suzuki, A.; Cheng, S.M.; Zon, G.; Liu, T.
J. Biol. Chem. 261, 10450-10455, 1986
A:Title: Isolation and characterization of Limulus C-reactive protein genes.
A:Reference number: A25551; MUID:86278105
A:Accession: A25192
A:Molecule type: DNA
A:Residues: 1-242 <NGU>
A:Cross-references: GB:M14024; NID:gl56631; PIDN:AAA28268.1; PID:gl56632
A:Note: the authors translated the codon ACC for residue 31 as Val
R:Nguyen, N.Y.; Suzuki, A.; Boykins, R.A.; Liu, T.Y.
J. Biol. Chem. 261, 10456-10465, 1986
A:Title: The amino acid sequence of Limulus C-reactive protein. Evidence of polymorph
A:Reference number: A25193; MUID:86278106
A:Accession: A25193
A:Molecule type: DNA
A:Residues: 25-242 <NG2>

C:Accession: C25192
R.Nguyen, N.Y.; Suzuki, A.; Cheng, S.M.; Zon, G.; Liu, T.
J. Biol. Chem. 261, 10450-10455, 1986
A:Title: Isolation and characterization of Limulus C-reactive protein genes.
A:Reference number: A92551; MUID:86278105
A:Accession: C25192
A:Molecule type: DNA
A:Residues: 1-242 <NGU>
A:Cross-references: GB:M14026; NID:gl55635; PIDN:AAA28270.1; PID:gl55636
C:Genetics:
A:Start codon: ATG.
C:Superfamily: C-reactive protein

Query Match 12.4%; Score 248.5; DB 2; Length 242;
Best Local Similarity 28.4%; Pred. No. 2.7e-12;
Matches 57; Conservative 44; Mismatches 91; Indels 9; Gaps 5;
QY 183 ILPPMRSKKIFGSHVPRPM-RLESPSACIWKATDVLNKLTLFSGYTKRNPVEIOLYLS 241
34 VKFPSSSPFPLVVMVGLPDLOEITLCYWFKNRLKGLHMFSTATAKKNELLTLD 93
QY 242 YQS--IVFVVGGENKLVAEAMVSLGRWTHLCOTWNSSEGLTSLWNG-ELAAATVEMAT 298
DB 94 EOGDFLNVHGAQLKVCQPNKTHIGKWHVCHTWSSEGEATIAVDGFCHKGNATGIAV 153
QY 299 GHIVPEGGILQIGERKNGCCVGGDETLAFSGRLTGFNIWDSVLSNEEIR---ETGGAE 355
DB 154 GRTLSGGGLVVLQGDQDS--VGGKFDATQSGELSELNWNVLNHEQIKYLSKCAHPS 211
QY 356 SCHIRNIVGWGVTEIQPHG 376
DB 212 ERHYGNIIQWDKTOFKAYDG 232

RESULT 9
A42579
C-reactive protein precursor - rat
N:Alternate names: CRP
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: A42579
R:Rassouli, M.; Sambasivam, H.; Azadi, P.; Dell, A.; Morris, H.R.; Nagpurkar, A.; Mooker
J. Biol. Chem. 267, 2947-2954, 1992
A:Title: Derivation of the amino acid sequence of rat C-reactive protein from cDNA clones
A:Reference number: A42579; MUID:92147634
A:Accession: A42579
A:Molecule type: mRNA
A:Residues: 1-230 <RAS>
A:Cross-references: GB:M83176; NID:g203591; PIDN:AAA40964.1; PID:g203592
A:Note: sequence extracted from NCBI backbone (NCBIP:80758)
C:Superfamily: C-reactive protein
C:Keywords: acute phase; liver; pentamer; pentraxin; plasma

Query Match 11.2%; Score 225.5; DB 2; Length 230;
Best Local Similarity 31.5%; Pred. No. 1.6e-10;
Matches 62; Conservative 32; Mismatches 90; Indels 13; Gaps 7;
QY 182 AILPPMRSKKIFGSHVPRPMRLESFACIWKATDVLNKLTLFSGYTKRNPVEIOLYLS 241
DB 27 AFVPGVSATAYVSLAESKKEAFVCLYAH-AVRSRFSIFSTATKTSFNEILLFWT 85
QY 242 Y-QSIVFVVGGENKLVAEAMVSLGRWTHLCOTWNSSEGLTSLWNGELAAATVEMATGH 300
DB 86 RGOGFSTAVGPELIFSASIEPEV--THICATWESATGIVELWLDGK-PRVRKSLOKGY 142
QY 301 IVPEGGILQIGERKNGCCVGGDETLAFSGRLTGFNIWDSVLSNEEIR--TGGAESCH 358
DB 143 IVGTNASIIILGQEQDS--YGGGFDANQSLVGDIGDVMNMDIVLSPEQINTVCVGGT-- 198
QY 359 IRGNIVGWGVTEIQPHG 375

DB 199 --PNVLNWRALKVETHG 213

RESULT 10
A40326
C-reactive protein precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1993
C:Accession: A40326; B40326
R:Dowton, S.B.; Hoiden, S.N.
Biochemistry 30, 9531-9538, 1991
A:Title: C-reactive protein (CRP) of the Syrian hamster.
A:Reference number: A40326; MUID:91369977
A:Accession: A40326
A:Molecule type: DNA
A:Residues: 1-225 <DOW>
A:Cross-references: GB:J05343; GB:S56005
A:Note: the authors translated the codon CTA for residue 199 as Asp and GAC for resid
A:Accession: B40326
A:Molecule type: mRNA
A:Residues: 1-225 <DOW>
A:Cross-references: GB:J05343; GB:S56005
C:Comment: This protein, unlike its homolog SAP (serum amyloid P component), is not g
C:Genetics:
A:Introns: 22/1
C:Superfamily: C-reactive protein
C:Keywords: pentamer
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-225/Product: C-reactive protein #status predicted <MAT>

Query Match 10.8%; Score 217.5; DB 2; Length 225;
Best Local Similarity 28.5%; Pred. No. 6.8e-10;
Matches 57; Conservative 38; Mismatches 92; Indels 13; Gaps 7;

QY 180 ETAILPPMRSKKIFGSHVPRPMRLESFACIWKATDVLNKLTLFSGYTKRNPVEIOL 238
DB 25 KTAFFPKESANSYVSLAESKKEAFVCLYAHITFELSTTRSFISYATKNSPNEILI 84
QY 239 YLSY-OSIVFVVGGENKLVAEAMVSLGRWTHLCOTWNSSEGLTSLWNGELAAATVEMA 297
DB 85 FWSKDRGYAFVGGPEVLKASIEPEV--THICASWESATGIAELWVDGKPKVKRI-LQ 141
QY 298 TGHIVPEGGILQIGERKNGCCVGGDETLAFSGRLTGFNIWDSVLSNEEIR--TGGAE 355
DB 142 KGYTVGTDASIIILGQEQDS--YGGGFDANQSLVGDIGDVMNMDIVLSPEQINTVCVGGT- 198
QY 356 SCHIRNIVGWGVTEIQPHG 375
DB 199 ---LDPSVLNWLQALKYVQG 215

RESULT 11
A45814
female protein precursor - Armenian hamster
C:Species: Cricetus migratorius (Armenian hamster)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C:Accession: A45814
R:Dowton, S.B.; Waggoner, D.J.
J. Immunol. 143, 3776-3780, 1989
A:Title: Armenian hamster female protein (serum amyloid P component). Comparison with
A:Reference number: A45814; MUID:90063074
A:Accession: A45814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <DOW>
A:Cross-references: GB:M31610; NID:gl91075; PIDN:AAA36981.1; PID:g304506
C:Superfamily: C-reactive protein

Query Match 10.6%; Score 212.5; DB 2; Length 231;
Best Local Similarity 28.7%; Pred. No. 1.8e-09;
Matches 58; Conservative 33; Mismatches 88; Indels 23; Gaps 6;

Qy 184 LFMRSKKIFGSHVPRMRLSEFSACIWKATDVNLKTLFSGYTKRNPYEIQLY----- 239
Db 29 VFPRESSESDYVKLPRLKPLENFTLC-FRTYTDLSRPHSLFSYNTKNDKELLIKERM 87
Qy 240 ----LSYOSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTLNVLVNGELAATVE 295
Db 88 GEYGLYIENLGAIVRGVE-----EFASPVHFCTSWESSGIAEFWNG-IPWVKKG 137
Qy 296 MATGHIIVEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFIWDSVLSNEIRETGAE 355
Db 138 LKKGTVTKTPSIILGQODN--YGGGFDKQSQFVGMDLNMWDSVLTPEIKSV--YE 193
Qy 356 SCHIRGNIVGNGVTEIQPHGA 377
Db 194 GSWLEANILDMRTLNYEMSGYA 215
RESULT 13
Query Match 10.5%; Score 211.5; DB 2; Length 223;
Best Local Similarity 28.7%; Pred. No. 2e-09;
Matches 58; Conservative 33; Mismatches 88; Indels 23; Gaps 6;
Qy 184 LFMRSKKIFGSHVPRMRLSEFSACIWKATDVNLKTLFSGYTKRNPYEIQLY----- 239
Db 29 VFPRESSESDYVKLPRLKPLENFTLC-FRTYTDLSRPHSLFSYNTKNDKELLIKERM 87
Qy 240 ----LSYOSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTLNVLVNGELAATVE 295
Db 88 GEYGLYIENLGAIVRGVE-----EFASPVHFCTSWESSGIAEFWNG-IPWVKKG 137
Qy 296 MATGHIIVEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFIWDSVLSNEIRETGAE 355
Db 138 LKKGTVTKTPSIILGQODN--YGGGFDKQSQFVGMDLNMWDSVLTPEIKSV--YE 193
Qy 356 SCHIRGNIVGNGVTEIQPHGA 377
Db 194 GSWLEANILDMRTLNYEMSGYA 215
RESULT 13
C-Reactive protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
C:Accession: A31583; S08286
R:Ohnishi, S.; Maeda, S.; Nishiguchi, S.; Arao, T.; Shimada, K.
Biochem. Biophys. Res. Commun. 156, 814-822, 1988
A:Title: Structure of the mouse C-reactive protein gene.
A:Reference number: A31583; MUID:89050112
A:Accession: A31583
A:Molecule type: DNA
A:Residues: 1-225 <OHN>

A:Cross-references: GB:X13588; NID:g50571; PIDN:CAA31928.1; PID:g295904
R:Whitehead, A.S.; Zahedi, K.; Rits, M.; Mortensen, R.F.; Lellias, J.M.
Biochem. J. 266, 283-290, 1990
A:Title: Mouse C-reactive protein. Generation of cDNA clones, structural analysis, an
A:Reference number: S08286; MUID:90179719
A:Accession: S08286
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-133; 'P', 135-225 <WHI>
A:Cross-references: EMBL:X17496; NID:g50563; PIDN:CAA35531.1; PID:g50564
C:Genetics:
A:Introns: 22/1
C:Superfamily: C-reactive protein
Query Match 10.1%; Score 203.5; DB 2; Length 225;
Best Local Similarity 27.6%; Pred. No. 8.7e-09;
Matches 55; Conservative 39; Mismatches 90; Indels 15; Gaps 9;
Qy 182 AILFPMRSKKIFGSHVPRMRLSEFSACI-WKATDVNLKTLFSGYTKRNPYEIQLYL 240
Db 27 AFVFPKESDTSYVSLAEASKKPLNTFTVCLHFTALSTVRSFVSFYATKKNSNDILIFW 86
Qy 241 SY-QSIVFVVGGEENKLVAEAMVSLGRWTHLCGTWNSEEGTLNVLVNGELAATTVEMATG 299
Db 87 NDKQYTFEGVGAERFVWSEIPEAP--THICASWESATGIVEFWIDCK-AKVRKSLHG 143
Qy 300 HIV-PEGGILQIGQKNGCCVGGGDFETLAFSGRLTGFIWDSVLSNEIRE--TGGAES 356
Db 144 YTVGPDSII-LGQODS--YGGDFDAKQSLVGDIGDYMNDVLSPEQINTVYVGGT-- 198
Qy 357 CHIRGNIVGNGVTEIQPHG 375
Db 199 --LSPNVLNWRALNYKAQG 215
RESULT 14
C-Reactive protein precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 05-Apr-1983 #sequence_revision 18-Jul-1997 #text_change 22-Jun-1999
C:Accession: A25605; A25583; A03202
R:Syn, C.; Gotschlich, E.C.; Liu, T.Y.
J. Biol. Chem. 261, 5473-5479, 1986
A:Title: Rabbit C-reactive protein. Biosynthesis and characterization of cDNA clones.
A:Reference number: A25605; MUID:86168292
A:Accession: A25605
A:Molecule type: mRNA
A:Residues: 1-225 <SVI>
A:Cross-references: GB:M13497; NID:g164901; PIDN:AAA31206.1; PID:g164902
R:Hu, S.I.; Miller, S.M.; Samols, D.
Biochemistry 25, 7834-7839, 1986
A:Title: Cloning and characterization of the gene for rabbit C-reactive protein.
A:Reference number: A25583; MUID:87101075
A:Accession: A25583
A:Molecule type: DNA
A:Residues: 1-9, 'T', 11-107, 'I', 109-192, 'I', 194-225 <HUS>
A:Cross-references: GB:M14538; NID:g164899; PIDN:AAA75403.1; PID:g164900
R:Wang, C.M.; Nguyen, N.Y.; Yonaha, K.; Robey, F.; Liu, T.Y.
J. Biol. Chem. 257, 13610-13615, 1982
A:Title: Primary structure of rabbit C-reactive protein.
A:Reference number: A03202; MUID:83056861
A:Accession: A03202
A:Molecule type: protein
A:Residues: 21-45, 'T', 47-49, 'L', 51-83, 'F', 85, 105, 'KE', 108, 'I', 110, 'Y', 112-166, 'W', 168
A:Note: 62-Lys and 108-Asp were also found
A:Note: Asp-61, Arg-76, Arg-77, and Glu-81 may be involved in the calcium-dependent b
C:Genetics:
A:Introns: 22/1
C:Superfamily: C-reactive protein
C:Keywords: acute phase; pentamer; plasma
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-225/Product: C-reactive protein #status experimental <MAT>

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:20 ; Search time 18.72 Seconds
(without alignments)
458.000 Million cell updates/sec

Title: us-09-555-473-1
Perfect score: 2007
Sequence: 1 MHLALFALMSAVLAENS.....NIVGNGVTETIQPHGGAQYVS 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

1 number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	788	39.3	178	1	US-07-929-580B-2
2	294	14.6	430	1	US-08-631-607-7
3	289.5	14.4	432	1	US-08-631-607-2
4	277	13.8	426	1	US-08-631-607-6
5	269.5	13.4	232	1	US-08-631-607-5
6	225.5	11.2	211	1	US-08-631-607-4
7	184.5	9.2	201	1	US-07-929-580B-3
8	184.5	9.2	225	1	US-07-708-885B-1
9	184.5	9.2	225	1	US-07-714-386-1
10	184.5	9.2	225	1	US-07-708-888A-1
11	183.5	9.1	208	1	US-08-631-607-3
12	160.5	8.0	201	1	US-07-929-580B-5
13	146.5	7.3	223	1	US-07-708-885B-3
14	146.5	7.3	223	1	US-07-714-386-3
15	146.5	7.3	223	1	US-07-708-888A-3
16	98.5	4.9	2101	1	US-08-466-390-4
17	98.5	4.9	2101	1	US-08-470-350-4
18	98.5	4.9	2101	1	US-08-467-781-4
19	98.5	4.9	2101	1	US-08-195-487-4
20	98.5	4.9	2101	2	US-08-483-924-4
21	98.5	4.9	2101	4	US-09-452-294-1
22	98.5	4.9	2101	5	PCT-US93-06160-4
23	98	4.9	2293	4	US-09-368-590-2
24	95.5	4.8	2627	2	US-08-751-189-3
25	95.5	4.8	2627	2	US-09-060-836-3
26	95.5	4.8	2627	4	US-09-184-445-3
27	91.5	4.6	280	1	US-08-781-562-4

28	91.5	4.6	566	2	US-08-533-669A-8	Sequence 8, Appl
29	91.5	4.6	566	2	US-08-511-872-2	Sequence 2, Appl
30	90.5	4.5	4545	2	US-08-804-227C-14	Sequence 14, Appl
31	90.5	4.5	4550	2	US-08-804-227C-8	Sequence 8, Appl
32	90.5	4.5	4550	2	US-08-804-198-2	Sequence 2, Appl
33	88	4.4	502	4	US-09-413-814-106	Sequence 106, App
34	88	4.4	2860	2	US-08-826-267-2	Sequence 2, Appl
35	87.5	4.4	3491	2	US-07-642-734C-2	Sequence 2, Appl
36	87.5	4.4	3491	3	US-08-439-009A-2	Sequence 2, Appl
37	87	4.3	897	1	US-08-095-737-4	Sequence 4, Appl
38	87	4.3	897	1	US-08-480-145-4	Sequence 4, Appl
39	87	4.3	897	2	US-08-477-389-4	Sequence 4, Appl
40	86	4.3	594	2	US-08-910-856-2	Sequence 2, Appl
41	86	4.3	5087	4	US-09-144-085-1	Sequence 1, Appl
42	84.5	4.2	341	1	US-08-190-802A-45	Sequence 45, Appl
43	84.5	4.2	341	4	US-08-477-346-45	Sequence 45, Appl
44	84.5	4.2	933	2	US-08-682-847-2	Sequence 2, Appl
45	84.5	4.2	2890	4	US-09-413-814-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-07-929-580B-2
; Sequence 2, Application US/07929580B
; Patent No. 5426181
; GENERAL INFORMATION:
; APPLICANT: Lee, Tae Ho
; APPLICANT: Lee, Gene W.
; APPLICANT: Vilcek, Jan
; TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
; TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION NUMBER: US/07929.580B
; FILING DATE: 19920814
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/640,492
; FILING DATE: 14-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Guy Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: LEE25\VLCEK-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-929-580B-2

Query Match 39.3%; Score 788; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MHLIAIFCALWSAVLAENSDDDYDLMYVNLIDNGLHPTDPTPCDCGQEHSEWDKLF 60
D 1 MHLIAIFCALWSAVLAENSDDDYDLMYVNLIDNGLHPTDPTPCDCGQEHSEWDKLF 60
QY 61 IMLENSQMRMLLQATDDYLVRLGELQRLREELGRLAESLARPCAPGAPAEARLTALSDEL 120
D 61 IMLENSQMRMLLQATDDYLVRLGELQRLREELGRLAESLARPCAPGAPAEARLTALSDEL 120
QY 121 LQATRDAGRRRLARMGAEAQRPPEAGRALAAVL 153
D 121 LQATRDAGRRRLARMGAEAQRPPEAGRALAAVL 153
RESULT 2
US-08-631-607-7
; Sequence 7, Application US/08631607
; Patent No. 5767252
; GENERAL INFORMATION:
; APPLICANT: Worley et al, Paul
; TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,607
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/086001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-631-607-7

```

```

QY 239 YLSYQSIVFVVGGEENKLVAE--AMVSLGRWTHLCGTWNSSEGLTSLWYNGELAAATTVM 290
Db 293 -----NDKVAQLPLFVSDGKWHHCIVTWTTRDGMWEAFQDGEKLGTEGL 337
QY 297 ATGHIVPEGGILOIQEKNGCCVGGGDETLAFSGRLTGFNIWDSVYLSNEEIRETGGAES 356
Db 338 APWHPINPGVGLILGQBD--TVGGREDATQAFVGLSQENIWDPLVFAQEIYVNIANC-S 394
QY 357 CHIRGNIVGMCVTEIQPHGGA 377
Db 395 TNMPGNLIIPWVSNNDVFGGA 415

RESULT 3
US-08-631-607-2
: Sequence 2, Application US/08631607
: Patent No. 5767252
: GENERAL INFORMATION:
: APPLICANT: Worley et al, Paul
: TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/631,607
: FILING DATE: 08-APR-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Haile, Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/DOCKET NUMBER: 07265/086001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 432 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-631-607-2

```

Query Match 14.6%; Score 294; DB 1; Length 430;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2001, 15:49:20 ; Search time 28.4 Seconds
(without alignments)
993.730 Million cell updates/sec

Title: US-09-555-473-1
Perfect score: 2007
Sequence: 1 MHLALIFCALNSAVLAENS.....NIVGWGVTEQPHGGAQYVS 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

al number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*

```

1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2007	100.0	381	20 AAY22803	Amino acid sequenc
2	1999	99.6	381	14 AAR42362	Pentaxin PTX3. Ho
3	1999	99.6	381	22 AAB90790	Human shear stress
4	788	39.3	178	13 AAR26181	TSG-14. Homo sapi
5	289.5	14.4	432	18 AAW31736	Neuronal activity-
6	289.5	14.4	432	22 AAB31178	Amino acid sequenc
7	278	13.9	502	22 AAU15114	Schizophrenia-asso
8	259.5	12.9	218	16 AAR74770	Limulus C-reactive
9	192	9.6	210	16 AAR74769	Female hamster pro
10	185.5	9.2	225	13 AAR29922	CRP. Homo sapiens
11	184.5	9.2	206	16 AAR74768	Human C-reactive p

12	184.5	9.2	206	18 AAW43405	Human C-reactive p
13	184.5	9.2	206	19 AAW40529	Human C-reactive p
14	184.5	9.2	206	20 AAW30582	Human C-reactive p
15	184.5	9.2	206	21 AAY76844	Human C-reactive p
16	167.5	8.3	204	16 AAR74763	Serum amyloid p c
17	152.5	7.6	203	22 AAB83050	Recombinant human
18	146.5	7.3	223	13 AAR29923	SAP. Homo sapiens
19	119	5.9	1316	22 AAB94754	Human protein sequ
20	115	5.7	689	22 AAU00713	Human novel G-prot
21	115	5.7	690	22 AAU00208	Human novel G-prot
22	115	5.7	690	22 AAU00717	Human novel G-prot
23	115	5.7	717	22 AAU00196	Human novel G-prot
24	115	5.7	718	22 AAU00192	Human novel G-prot
25	115	5.7	718	22 AAU00200	Human novel G-prot
26	115	5.7	1083	22 AAU00714	Human novel G-prot
27	115	5.7	1084	22 AAU00209	Human novel G-prot
28	115	5.7	1084	22 AAU00718	Human novel G-prot
29	115	5.7	1111	22 AAU00197	Human novel G-prot
30	115	5.7	1112	22 AAU00193	Human novel G-prot
31	115	5.7	1112	22 AAU00201	Human novel G-prot
32	115	5.7	1192	22 AAU00712	Human novel G-prot
33	115	5.7	1192	22 AAU00719	Human novel G-prot
34	115	5.7	1193	22 AAU00207	Human novel G-prot
35	115	5.7	1193	22 AAU00716	Human novel G-prot
36	115	5.7	1220	22 AAU00195	Human novel G-prot
37	115	5.7	1221	22 AAU00191	Human novel G-prot
38	115	5.7	1221	22 AAU00199	Human novel G-prot
39	115	5.7	1221	22 AAU00210	Human novel G-prot
40	115	5.7	1222	22 AAU00206	Human novel G-prot
41	115	5.7	1222	22 AAU00715	Human novel G-prot
42	115	5.7	1249	22 AAU00194	Human novel G-prot
43	115	5.7	1250	22 AAU00190	Human novel G-prot
44	115	5.7	1250	22 AAU00198	Human novel G-prot
45	114	5.7	532	21 AAB42542	Human ORFX ORF2306

ALIGNMENTS

```

RESULT 1
AAV22803
ID AAY22803 standard; Protein; 381 AA.
XX
AC AAY22803;
XX
DT 26-AUG-1999 (first entry)
XX
DE Amino acid sequence of human long pentraxin (PTX3).
XX
KW Human; long pentraxin; PTX3; gene therapy; cancer; infectious disease;
KW inflammatory disease; tumour disease; anticancer.
XX
OS Homo sapiens.
XX
XX WO9932516-A2.
XX
PD 01-JUL-1999.
XX
PF 16-DEC-1998; 98WO-IT00364.
XX
PR 19-DEC-1997; 97IT-RM00796.
XX
(SICT) SIGMA-TAU IND FARM RIUNITE SPA.
PA
PI Bottazzi B, Introna M, Mantovani A, Vecchi A;
XX
DR WPI; 1999-405159/34.
DR N-PSDB; AAX81675.
XX
PT New pharmaceutical compositions containing pentraxin (PTX3), useful
PT for treating infectious and inflammatory diseases or tumours
XX
PS Diselourse; Page 22-24; 26pp; English.

```

XX The present sequence represents human long pentaxin (PTX3). The
CC specification describes pharmaceutical compositions comprising PTX3.
CC The PTX3 expression vector is useful in gene therapy for treating
CC cancer sufferers, especially as an adenovirus or retrovirus. The
CC PTX3 is also useful for preparing a medicament for the treatment of
CC infectious, inflammatory or tumour diseases. The anticancer activity
CC of PTX3 enables it to be of therapeutic use in treating infectious,
CC inflammatory and tumour diseases.
XX
SQ Sequence 381 AA;

Query Match 100.0%; Score 2007; DB 20; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.7e-189;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHLAILFCAWSAVLAENSDYDLMYVNLNDEIDNGLHPTEDPTPCDQGBHSEWDLKF 60
1 mhlailfcalwsavlaensddydlmyvnlndneidnglhptedptpcdgcgqehsewdklf 60
61 IMLENSQMRERMLLQATDDVLRGELQRLREELGRLAESLARPCAPGAPAEARLTALDEL 120
61 imlensqmrermllqatddvlrgelqrleelgrlaeslarpcapgapaearltsaldel 120
QY 121 LQATRDAGRRLARMEGAERPEEAGRALAAVLEELRQTRADLHVOGWAARSWLPAGCE 180
121 lqatrdagrllarmegaeaqrpееagrалaaVleelrqtradlhavogwaarswlpagce 180
QY 181 TAILFPMRSKKIFGSHVPRPMLRLESFSACIWKATDVLNKTILFSYGTGRNPYEIQLYL 240
181 tailfpmrskkifgshvprpmlrlesfsaciwkvatdvlnktilfsygtkrnpyeiqlyl 240
QY 241 SYQSIVFVVGGEENKLVAAEMVSLGRWTHLCGTWNSEEGITSLWNGELAATTVMATCH 300
241 syqsivfvvggeenkvlvaamvslgrwthlctwnseegitslwngelaattvmatch 300
QY 301 IYPEGGILQIGQKNGCCVGGGFDETLAFSGRLTGFIWDSVLSNEEIRETGGAESCHIR 360
301 iypeggilqigqkngccvvggfdeTLafsgrltgfiwdsVlsneeiretggaeschir 360
QY 361 GNIVGWGVTEIQPHGGAQYVS 381
361 gnivgwgvtelqphggaqyvs 381

RESULT 2
AAR42362
AAR42362 standard; Protein; 381 AA.
AAR42362.
18-APR-1994 (first entry)
Pentaxin PTX3.
Independent tissue stress indicator; interleukin; IL-1; TNF-alpha;
tissue necrosis factor; hepatocyte.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..18
/note= "signal peptide"
Peptide 269..276
/note= "characteristic of pentaxin family"
Peptide 272..281
/note= "used to produce monoclonal antibodies"
W09321313-A.
28-OCT-1993.

PF 08-APR-1993; 93WO-EF00868.
XX
PR 14-APR-1992; 92IT-OMI0901.
XX
PA (MODE/) MODENA D.
PA (ITAF) ITALFARMACO SPA.
XX
PI Breviario F, Dejana E, Introna M, Legname G, Mantovani A;
PI Modenad D;
XX
DR WPI; 1993-351723/44.
DR N-PSDB; AAQ51036.
XX
PT Sequence for gene of pentaxin family - expressed in cells other
PT than hepatocytes and may serve as independent tissue stress
PT indicator
XX
PS Claim 9; Fig 3; 2lpp; English.
XX
CC A cDNA library was constructed in lambda ZAP from total RNA isolated
CC from human umbilical vein endothelial cells exposed for 1 hour to
CC interleukin-1. The library was differentially screened with cDNA
CC probes from untreated versus IL-1 treated HUVEC. The positive clone
CC isolated was found to be a new gene, termed PTX3. This gene encodes a
CC product showing close homology to members of the pentaxin family.
CC The gene is strongly induced by TNF-alpha and IL-1 but not IL-6 so
CC may provide an independent indication of tissue stress in most
CC tissue types since it is expressed in cells other than hepatocytes.
XX
SQ Sequence 381 AA;

Query Match 99.6%; Score 1999; DB 14; Length 381;
Best Local Similarity 99.7%; Pred. No. 2.9e-188;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHLAILFCAWSAVLAENSDYDLMYVNLNDEIDNGLHPTEDPTPCDQGBHSEWDLKF 60
1 mhlailfcalwsavlaensddydlmyvnlndneidnglhptedptpcdgcgqehsewdklf 60
DB 1 mhlailfcalwsavlaensddydlmyvnlndneidnglhptedptpcacqgqehsewdklf 60
QY 61 IMLENSQMRERMLLQATDDVLRGELQRLREELGRLAESLARPCAPGAPAEARLTALDEL 120
61 imlensqmrermllqatddvlrgelqrleelgrlaeslarpcapgapaearltsaldel 120
DB 61 imlensqmrermllqatddvlrgelqrleelgrlaeslarpcapgapaearltsaldel 120
QY 121 LQATRDAGRRLARMEGAERPEEAGRALAAVLEELRQTRADLHVOGWAARSWLPAGCE 180
121 lqatrdagrllarmegaeaqrpееagrалaaVleelrqtradlhavogwaarswlpagce 180
DB 121 lqatrdagrllarmegaeaqrpееagrалaaVleelrqtradlhavogwaarswlpagce 180
QY 181 TAILFPMRSKKIFGSHVPRPMLRLESFSACIWKATDVLNKTILFSYGTGRNPYEIQLYL 240
181 tailfpmrskkifgshvprpmlrlesfsaciwkvatdvlnktilfsygtkrnpyeiqlyl 240
DB 181 tailfpmrskkifgshvprpmlrlesfsaciwkvatdvlnktilfsygtkrnpyeiqlyl 240
QY 241 SYQSIVFVVGGEENKLVAAEMVSLGRWTHLCGTWNSEEGITSLWNGELAATTVMATCH 300
241 syqsivfvvggeenkvlvaamvslgrwthlctwnseegitslwngelaattvmatch 300
DB 241 syqsivfvvggeenkvlvaamvslgrwthlctwnseegitslwngelaattvmatch 300
QY 301 IYPEGGILQIGQKNGCCVGGGFDETLAFSGRLTGFIWDSVLSNEEIRETGGAESCHIR 360
301 iypeggilqigqkngccvvggfdeTLafsgrltgfiwdsVlsneeiretggaeschir 360
DB 301 iypeggilqigqkngccvvggfdeTLafsgrltgfiwdsVlsneeiretggaeschir 360
QY 361 GNIVGWGVTEIQPHGGAQYVS 381
361 gnivgwgvtelqphggaqyvs 381
DB 361 gnivgwgvtelqphggaqyvs 381

RESULT 3
AAB90790
ID AAB90790 standard; Protein; 381 AA.
XX
AC AAB90790;
XX
DT 15-JUN-2001 (first entry)
XX